

SEQUENCE LISTING

- <110> Hauptmann, Rudolph Himmler, Adolph Maurer-Fogy, Ingrid Stratowa, Christian
- <120> TNF Receptors, TNF Binding Proteins and DNAs Coding for $$\operatorname{\textbf{Them}}$$
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- <150> 09/525,998
- <151> 2000-03-15
- <150> 08/383,676
- <151> 1995-02-01
- <150> 08/153,287
- <151> 1993-11-17
- <150> 07/821,750
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- <160> 97
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Tyr Ile His Pro Gln Asn Asn Ser Ile Cys Cys Thr Lys Cys His Lys 50 55 60

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Cys Arg Glu Cys Glu Ser Gly Ser Phe Thr Ala Ser Glu Asn His Leu 85 90 95

Arg His Cys Leu Ser Cys Ser Lys Cys Arg Lys Glu Met Gly Gln Val 100 105 110

Glu Ile Ser Ser Cys Thr Val Asp Arg Asp Thr Val Cys Gly Cys Arg 115 120 125

Lys Asn Gln Tyr Arg His Tyr Trp Ser Glu Asn Leu Phe Gln Cys Phe 130 135 140

Asn Cys Ser Leu Cys Leu Asn Gly Thr Val His Leu Ser Cys Gln Glu 145 150 155 160

Lys Gln Asn Thr Val Cys Thr Cys His Ala Gly Phe Phe Leu Arg Glu 165 170 175

Asn Glu Cys Val Ser Cys Ser Asn Cys Lys Lys Ser Leu Glu Cys Thr 180 185 190

Lys Leu Cys Leu Pro Gln Ile Glu Asn Val Lys Gly Thr Glu Asp Ser 195 200 205

Gly Thr Thr Val Leu Leu Pro Leu Val Ile Phe Phe Gly Leu Cys Leu 210 215 220

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acc Thr																384
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Pro	Gly	Pro 35	Gly	Gln	Asp	Thr	Asp 40	Cys	Arg	Glu	Cys	Glu 45	Ser	Gly	Ser	
Phe	Thr 50	Ala	Ser	Glu	Asn	His 55	Leu	Arg	His	Cys	Leu 60	Ser	Cys	Ser	Lys	

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Ser	Glu	Asn	Leu 100	Phe	Gln	Cys	Phe	Asn 105	Cys	Ser	Leu	Cys	Leu 110	Asn	Gly	
Thr	Val	His 115	Leu	Ser	Cys	Gln	Glu 120	Lys	Gln	Asn	Thr	Val 125	Cys	Thr	Cys	
His	Ala 130	Gly	Phe	Phe	Leu	Arg 135	Glu	Asn	Glu	Cys	Val 140	Ser	Cys	Ser	Asn	
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cac cta ggg gac agg gag aag aga gat agt gtg tgt ccc caa gga aaa 144 His Leu Gly Asp Arg Glu Lys Arg Asp Ser Val Cys Pro Gln Gly Lys 35 40 45
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Phe	Gln	Cys 115	Phe	Asn	Cys	Ser	Leu 120	Cys	Leu	Asn	Gly	Thr 125	Val	His	Leu	
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11	y Cys Ar	J Lys		Gln 120	Tyr	Arg	His	Tyr	Trp 125	Ser	Glu	Asn	
Leu Phe Gl 130	n Cys Ph	e Asn	Cys 135	Ser	Leu	Cys	Leu	Asn 140	Gly	Thr	Val	His	
Leu Ser Cy 145	s Gln Gl	ı Lys 150	Gln	Asn	Thr	Val	Cys 155	Thr	Cys	His	Ala	Gly 160	
Phe Phe Le	ı Arg Gl		Glu	Cys	Val	Ser 170	Cys	Ser	Asn	Cys	Lys 175	Lys	
Ser Leu Gl	1 Cys Th	r Lys	Leu		Leu 185	Pro	Gln	Ile	Glu	Asn 190	Val	Lys	
Gly Thr Gl 19	-	r Gly		Thr 200									
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000													
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	cac His															336
	atc Ile			_			_		_							384
	aac Asn 130															432
	tgc Cys															480
	cag Gln															528
	gag Glu	_	-													576
	ttg Leu															603
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	0> 14 Gly		Ser	Thr 5	Val	Pro	Asp	Leu	Leu 10	Leu	Pro	Leu	Val	Leu 15	Leu	
Glu	Leu	Leu	Val 20	Gly	Ile	Tyr	Pro	Ser 25	Gly	Val	Ile	Gly	Leu 30	Val	Pro	
His	Leu	Gly 35	Asp	Arg	Glu	Lys	Arg 40	Asp	Ser	Val	Cys	Pro 45	Gln	Gly	Lys	
Tyr	Ile 50	His	Pro	Gln	Asn	Asn 55	Ser	Ile	Cys	Суз	Thr 60	Lys	Cys	His	Lys	
Gly 65	Thr	Tyr	Leu	Tyr	Asn 70	Asp	Суѕ	Pro	Gly	Pro 75	Gly	Gln	Asp	Thr	Asp 80	
Cys	Arg	Glu	Cys	Glu 85	Ser	Gly	Ser	Phe	Thr 90	Ala	Ser	Glu	Asn	His 95	Leu	

	Leu Ser 100	Cys S	er Lys	Cys 105	Arg	Lys	Glu	Met	Gly 110	Gln	Val	
Glu Ile Ser 115	Ser Cys	Thr V	al Asp 120	Arg	Asp	Thr	Val	Cys 125	Gly	Cys	Arg	
Lys Asn Gln 130	Tyr Arg		yr Trp 35	Ser	Glu	Asn	Leu 140	Phe	Gln	Cys	Phe	
Asn Cys Ser 145	Leu Cys	Leu A 150	sn Gly	Thr	Val	His 155	Leu	Ser	Cys	Gln	Glu 160	
Lys Gln Asn	Thr Val 165	Суѕ Т	hr Cys		Ala 170	Gly	Phe	Phe	Leu	Arg 175	Glu	
Asn Glu Cys	Val Ser 180	Cys S	er Asn	Cys 185	Lys	Lys	Ser	Leu	Glu 190	Cys	Thr	
Lys Leu Cys 195	Leu Pro	Gln I	le Glu 200	Asn								
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atg gg Met Gl															288
tgt gg Cys Gl															336
ttc ca Phe Gl		Phe													384
tcc to Ser Cy 13	s Glr														432
ttt ct Phe Le 145															480
ctg ga Leu Gl															519
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\Z13/	ALCII	icia.	l Sec	quen	ce										
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Ser Cys Gln Glu Lys Gln Asn Thr Val Cys Thr Cys His Ala Gly Phe 130 135 140	
Phe Leu Arg Glu Asn Glu Cys Val Ser Cys Ser Asn Cys Lys Lys Ser 145 150 155 160	
Leu Glu Cys Thr Lys Leu Cys Leu Pro Gln Ile Glu Asn 165 170	
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gag ctg ttg gtg gga ata tac ccc tca ggg gtt att gga gat agt gtg 96 Glu Leu Leu Val Gly Ile Tyr Pro Ser Gly Val Ile Gly Asp Ser Val 20 25 30	
tgt ccc caa gga aaa tat atc cac cct caa aat aat tcg att tgc tgt Cys Pro Gln Gly Lys Tyr Ile His Pro Gln Asn Asn Ser Ile Cys Cys 35 40 45	4
acc aag tgc cac aaa gga acc tac ttg tac aat gac tgt cca ggc ccg Thr Lys Cys His Lys Gly Thr Tyr Leu Tyr Asn Asp Cys Pro Gly Pro 50 55 60	2
ggg cag gat acg gac tgc agg gag tgt gag agc ggc tcc ttc acc gct Gly Gln Asp Thr Asp Cys Arg Glu Cys Glu Ser Gly Ser Phe Thr Ala 65 70 75 80	0
tca gaa aac cac ctc aga cac tgc ctc agc tgc tcc aaa tgc cga aag 288 Ser Glu Asn His Leu Arg His Cys Leu Ser Cys Ser Lys Cys Arg Lys 85 90 95	8
gaa atg ggt cag gtg gag atc tct tct tgc aca gtg gac cgg gac acc Glu Met Gly Gln Val Glu Ile Ser Ser Cys Thr Val Asp Arg Asp Thr 100 105 110	6
gtg tgt ggc tgc agg aag aac cag tac cgg cat tat tgg agt gaa aac Val Cys Gly Cys Arg Lys Asn Gln Tyr Arg His Tyr Trp Ser Glu Asn 115 120 125	4

ctt ttc cag tgc ttc aat tgc agc ctc tgc ctc aat ggg acc gtg cac Leu Phe Gln Cys Phe Asn Cys Ser Leu Cys Leu Asn Gly Thr Val His 130 135 140	!
ctc tcc tgc cag gag aaa cag aac acc gtg tgc acc tgc cat gca ggt Leu Ser Cys Gln Glu Lys Gln Asn Thr Val Cys Thr Cys His Ala Gly 145 150 155 160	}
ttc ttt cta aga gaa aac gag tgt gtc tcc tgt agt aac tgt aag aaa 528 Phe Phe Leu Arg Glu Asn Glu Cys Val Ser Cys Ser Asn Cys Lys Lys 165 170 175	}
agc ctg gag tgc acg aag ttg tgc cta ccc cag att gag aat Ser Leu Glu Cys Thr Lys Leu Cys Leu Pro Gln Ile Glu Asn 180 185 190)
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Cys Pro Gln Gly Lys Tyr Ile His Pro Gln Asn Asn Ser Ile Cys Cys 35 40 45	
Thr Lys Cys His Lys Gly Thr Tyr Leu Tyr Asn Asp Cys Pro Gly Pro 50 55 60	
Gly Gln Asp Thr Asp Cys Arg Glu Cys Glu Ser Gly Ser Phe Thr Ala 65 70 75 80	
Ser Glu Asn His Leu Arg His Cys Leu Ser Cys Ser Lys Cys Arg Lys 85 90 95	
Glu Met Gly Gln Val Glu Ile Ser Ser Cys Thr Val Asp Arg Asp Thr	
Val Cys Gly Cys Arg Lys Asn Gln Tyr Arg His Tyr Trp Ser Glu Asn 115 120 125	
Leu Phe Gln Cys Phe Asn Cys Ser Leu Cys Leu Asn Gly Thr Val His 130 135 140	
Leu Ser Cys Gln Glu Lys Gln Asn Thr Val Cys Thr Cys His Ala Gly 145 150 155 160	

Phe Phe Leu Arg Glu Asn Glu Cys Val Ser Cys Ser Asn Cys Lys Lys 165 170 175

Ser Leu Glu Cys Thr Lys Leu Cys Leu Pro Gln Ile Glu Asn 180 185 190

<210> 19

<211> 516

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: recombinant TNF-BP sequence

<220>

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<222> (1)..(516)

<400> 19

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Ser Ile Cys Cys Thr Lys Cys His Lys Gly Thr Tyr Leu Tyr Asn Asp
20 25 30

tgt cca ggc ccg ggg cag gat acg gac tgc agg gag tgt gag agc ggc 144
Cys Pro Gly Pro Gly Gln Asp Thr Asp Cys Arg Glu Cys Glu Ser Gly
35 40 45

tcc ttc acc gct tca gaa aac cac ctc aga cac tgc ctc agc tgc tcc 192
Ser Phe Thr Ala Ser Glu Asn His Leu Arg His Cys Leu Ser Cys Ser
50 55 60

aaa tgc cga aag gaa atg ggt cag gtg gag atc tct tct tgc aca gtg 240 Lys Cys Arg Lys Glu Met Gly Gln Val Glu Ile Ser Ser Cys Thr Val 65 70 75 80

gac cgg gac acc gtg tgt ggc tgc agg aag aac cag tac cgg cat tat 288
Asp Arg Asp Thr Val Cys Gly Cys Arg Lys Asn Gln Tyr Arg His Tyr

tgg agt gaa aac ctt ttc cag tgc ttc aat tgc agc ctc tgc ctc aat 336
Trp Ser Glu Asn Leu Phe Gln Cys Phe Asn Cys Ser Leu Cys Leu Asn
100 105 110

ggg acc gtg cac ctc tcc tgc cag gag aaa cag aac acc gtg tgc acc 384
Gly Thr Val His Leu Ser Cys Gln Glu Lys Gln Asn Thr Val Cys Thr
115 120 125

tgc cat gca ggt ttc ttt cta aga gaa aac gag tgt gtc tcc tgt agt 432 Cys His Ala Gly Phe Phe Leu Arg Glu Asn Glu Cys Val Ser Cys Ser 130 135 140

aac tgt aag aaa agc ctg gag tgc acg aag ttg tgc cta ccc cag att Asn Cys Lys Lys Ser Leu Glu Cys Thr Lys Leu Cys Leu Pro Gln Ile 145 150 155 160
gag aat gtt aag ggc act gag gac tca ggc acc aca Glu Asn Val Lys Gly Thr Glu Asp Ser Gly Thr Thr 165 170
<210> 20 <211> 172 <212> PRT <213> Artificial Sequence
<220> <223> Description of Artificial Sequence: recombinant TNF-BP sequence
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Cys Pro Gly Pro Gly Gln Asp Thr Asp Cys Arg Glu Cys Glu Ser Gly 35 40 45
Ser Phe Thr Ala Ser Glu Asn His Leu Arg His Cys Leu Ser Cys Ser 50 55 60
Lys Cys Arg Lys Glu Met Gly Gln Val Glu Ile Ser Ser Cys Thr Val 65 70 75 80
Asp Arg Asp Thr Val Cys Gly Cys Arg Lys Asn Gln Tyr Arg His Tyr 85 90 95
Trp Ser Glu Asn Leu Phe Gln Cys Phe Asn Cys Ser Leu Cys Leu Asn 100 105 110
Gly Thr Val His Leu Ser Cys Gln Glu Lys Gln Asn Thr Val Cys Thr 115 120 125
Cys His Ala Gly Phe Phe Leu Arg Glu Asn Glu Cys Val Ser Cys Ser 130 135 140
Asn Cys Lys Lys Ser Leu Glu Cys Thr Lys Leu Cys Leu Pro Gln Ile 145 150 155 160

Glu Asn Val Lys Gly Thr Glu Asp Ser Gly Thr Thr

165

480

516

<210> 21 <211> 1334 <212> DNA 170

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<213> Artificial Sequence

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_		_				cta Leu										761
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						gag Glu										857
_	_					ctt Leu	-									905
						cgg Arg										953
						gaa Glu										1001
Thr						aac Asn 270										1049
			-			agt Ser				_						1097
						ggt Gly										1145
						tat Tyr										1193
•		~		_		atc Ile					_	_			_	1241
-	_		-		_	agc Ser 350		-								1289
	_					gtg Val		_	_	_		aagg	gaati	cc		1334

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220> 223> Description of Artificial Sequence: cDNA insert of lambdaTNF-BP15 and pTNF-BP15 vectors
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Glu Leu Leu Val Gly Ile Tyr Pro Ser Gly Val Ile Gly Leu Val Pro 20 25 30
His Leu Gly Asp Arg Glu Lys Arg Asp Ser Val Cys Pro Gln Gly Lys 35 40 45
Cyr Ile His Pro Gln Asn Asn Ser Ile Cys Cys Thr Lys Cys His Lys 50 55 60
Gly Thr Tyr Leu Tyr Asn Asp Cys Pro Gly Pro Gly Gln Asp Thr Asp 65 70 75 80
Cys Arg Glu Cys Glu Ser Gly Ser Phe Thr Ala Ser Glu Asn His Leu 85 90 95
Arg His Cys Leu Ser Cys Ser Lys Cys Arg Lys Glu Ile Gly Gln Val
Glu Ile Ser Ser Cys Thr Val Asp Arg Asp Thr Val Cys Gly Cys Arg 115 120 125
Lys Asn Gln Tyr Arg His Tyr Trp Ser Glu Asn Leu Phe Gln Cys Phe 130 135 140
Asn Cys Ser Leu Cys Leu Asn Gly Thr Val His Leu Ser Cys Gln Glu 150 155 160
Lys Gln Asn Thr Val Cys Thr Cys His Ala Gly Phe Phe Leu Arg Glu 165 170 175
Asn Glu Cys Val Ser Cys Ser Asn Cys Lys Lys Ser Leu Glu Cys Arg 180 185 190
Lys Leu Cys Leu Pro Gln Ile Glu Asn Val Lys Gly Thr Glu Asp Ser 195 200 205
Gly Thr Thr Val Leu Leu Pro Leu Val Ile Phe Phe Gly Leu Cys Leu 210 220
Leu Ser Leu Leu Phe Ile Gly Leu Met Tyr Arg Tyr Gln Arg Trp Lys 225 230 235 240
Ser Lys Leu Tyr Ser Ile Val Cys Gly Lys Ser Thr Pro Glu Lys Glu 245 250 255

Gly Glu Leu Glu Gly Thr Thr Lys Pro Leu Ala Pro Asn Pro Ser 265 Phe Ser Pro Thr Pro Gly Phe Thr Pro Thr Leu Gly Phe Ser Pro Val 280 Pro Ser Ser Thr Phe Thr Ser Ser Ser Thr Tyr Thr Pro Gly Asp Cys 300 295 Pro Asn Phe Ala Ala Pro Arg Glu Val Ala Pro Pro Tyr Gln Gly Ala Asp Pro Ile Leu Ala Thr Ala Leu Ala Ser Asp Pro Ile Pro Asn 330 335 325 Pro Leu Gln Lys Trp Glu Asp Ser Ala His Lys Pro Gln Ser Leu Asp 345 Thr Asp Asp Pro Ala Thr Leu Tyr Ala Val Val Glu Asn Val Pro Pro 360 Leu Arg Trp 370 <210> 23 <211> 6414 <212> DNA <213> Artificial Sequence <220> <223> Description of Artificial Sequence: pADCMV1 vector <220> <221> unsure <222> (344) <223> "n" can be a, g, c, or t <220> <221> unsure <222> (4157) <223> "n" can be a, g, c, or t <220> <221> unsure <222> (5135) <223> "n" can be a, g, c, or t <220> <221> unsure <222> (6255) <223> "n" can be a, g, c, or t tcgacattga ttattgacta gttattaata gtaatcaatt acggggtcat tagttcatag 60 cccatatatg gagttccgcg ttacataact tacggtaaat ggcccgcctc gctgaccgcc 120 caacqacccc cqcccattqa cqtcaataat gacqtatqtt cccataqtaa cqccaataqg 180 gactttccat tgacgtcaat gggtggagta tttacggtaa actgcccact tggcagtaca 240 tcaagtgtat catatgccaa gtacgccccc tattgacgtc aatgacggta aatggcccgc 300 ctggcattat gcccagtaca tgaccttatg ggactttcct actnggcagt acatctacgt 360 attagtcatc gctattacca tggtgatgcg gttttggcag tacatcaatg ggcgtggata 420 gcggtttgac tcacggggat ttccaagtct ccaccccatt gacgtcaatg ggagtttgtt 480 ttggcaccaa aatcaacggg actttccaaa atgtcgtaac aactccgccc cattgacgca 540 aatgggcggt aggcgtgtac ggtgggaggt ctatataagc agagctctct ggctaactag 600 agaacccact gcttaactgg cttatcgaaa ttaatacgac tcactatagg gagacccaag 660 cttctgcagg tcgacatcga tggatccggt acctcgagcg cgaattctct agaggatctt 720 tgtgaaggaa ccttacttct gtggtgtgac ataattggac aaactaccta cagagattta 780 aagctctaag gtaaatataa aatttttaag tgtataatgt gttaaactac tgattctaat 840 tgtttgtgta ttttagattc caacctatgg aactgatgaa tgggagcagt ggtggaatgc 900 ctttaatgag gaaaacctgt tttgctcaga agaaatgcca tctagtgatg atgaggctac 960 tgctgactct caacattcta ctcctccaaa aaagaagaga aaggtagaag accccaagga 1020 ctttccttca gaattgctaa gttttttgag tcatgctgtg tttagtaata gaactcttgc 1080 ttgctttgct atttacacca caaaggaaaa agctgcactg ctatacaaga aaattatgga 1140 aaaatatttg atgtatagtg cettgactag agateataat eagecatace acatttgtag 1200 aggttttact tgctttaaaa aacctcccac acctcccct gaacctgaaa cataaaatga 1260 atgcaattgt tgttgttaac ttgtttattg cagcttataa tggttacaaa taaagcaata 1320 gcatcacaaa tttcacaaat aaagcatttt tttcactgca ttctagttgt ggtttgtcca 1380 aactcatcaa tgtatcttat catgtctgga tcaattctga gaaactagcc ttaaagacag 1440 acagctttgt tctagtcagc caggcaagca tatgtaaata aagttcctca gggaactgag 1500 gttaaaagat gtatcctgga cctgccagac ctggccattc acgtaaacag aagattccgc 1560 ctcaagttcc ggttaacaac aggaggcaac gagatctcaa atctattact tctaatcggg 1620 taattaaaac ctttcaacta aaacacggac ccacggatgt cacccacttt tccttccccg 1680 geteegeest teteagtact ecceaecatt aggetegeta eteeaectee aetteeggge 1740 gcgacaccca cgtgccctct cccacccgac gctaaccccg ccctgcccg tctgaccccg 1800

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								ctg Leu				961
			_					agg Arg				1009
								aag Lys 265				1057
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	_		-	-				gag Glu				1441
	_	_		_		_		agc Ser				1489
cgc Arg								ctg				1537

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Tyr Ala His Pro Lys Asn Asn Ser Ile Cys Cys Thr Lys Cys His Lys 50 55 60

Gly Thr Tyr Leu Val Ser Asp Cys Pro Ser Pro Gly Gln Glu Thr Val 65 70 75 80

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-		_			ttt Phe		-	-								761
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Glu Leu Leu V	Val Gly Ile 20	Tyr Pro	Ser Gly 25	Val Ile	Gly Leu 30	Val Pro
His Leu Gly 35	Asp Arg Glu	Lys Arg 40	Asp Ser	Val Cys	Pro Gln 45	Gly Lys
Tyr Ile His 1	Pro Gln Asn	Asn Ser 55	Ile Cys	Cys Thr 60	Lys Cys	His Lys
Gly Thr Tyr 1	Leu Tyr Asn 70	Asp Cys	Pro Gly	Pro Gly 75	Gln Asp	Thr Asp
Cys Arg Glu	Cys Glu Ser 85	Gly Ser	Phe Thr	Ala Ser	Glu Asn	His Leu 95
Arg His Cys	Leu Ser Cys 100	Ser Lys	Cys Arg 105	Lys Glu	Met Gly	
Glu Ile Ser : 115	Ser Cys Thr	Val Asp 120	Arg Asp	Thr Val	Cys Gly 125	Cys Arg
Lys Asn Gln '	Tyr Arg His	Tyr Trp 135	Ser Glu	Asn Leu 140	Phe Gln	Cys Phe
Asn Cys Ser 1	Leu Cys Leu 150	Asn Gly	Thr Val	His Leu 155	Ser Cys	Gln Glu 160
Lys Gln Asn '	Thr Val Cys 165	Thr Cys	His Ala 170	Gly Phe	Phe Leu	Arg Glu 175
Asn Glu Cys	Val Ser Cys 180	Ser Asn	Cys Lys 185	Lys Ser	Leu Glu 190	Cys Thr
Lys Leu Cys 1	Leu Pro Gln	Ile Glu 200	Asn Val	Lys Gly	Thr Glu 205	Asp Ser
Gly Thr Thr 1	Val Leu Leu	Pro Leu 215	Val Ile	Phe Phe 220	Gly Leu	Cys Leu
Leu Ser Leu 2 225	Leu Phe Ile 230	Gly Leu	Met Tyr	Arg Tyr 235	Gln Arg	Trp Lys 240
Ser Lys Leu '	Tyr Ser Ile 245	Val Cys	Gly Lys 250	Ser Thr	Pro Glu	Lys Glu 255

Gly Glu Leu Glu Gly Thr Thr Lys Pro Leu Ala Pro Asn Pro Ser

			260					265					270		
Phe	Ser	Pro	Thr	Pro	Gly	Phe	Thr	Pro	Thr	Leu	Gly	Phe	Ser	Pro	Val

275 280 285

Pro Ser Ser Thr Phe Thr Ser Ser Ser Thr Tyr Thr Pro Gly Asp Cys 290 295 300

Pro Asn Phe Ala Ala Pro Arg Arg Glu Val Ala Pro Pro Tyr Gln Gly 305 310 315 320

Ala Asp Pro Ile Leu Ala Thr Ala Leu Ala Ser Asp Pro Ile Pro Asn 325 330 335

Pro Leu Gln Lys Trp Glu Asp Ser Ala His Lys Pro Gln Ser Leu Asp 340 345 350

Thr Asp Asp Pro Ala Thr Leu Tyr Ala Val Val Glu Asn Val Pro Pro 355 360 365

Leu Arg Trp Lys Glu Phe Val Arg Arg Leu Gly Leu Ser Asp His Glu 370 380

Ile Asp Arg Leu Glu Leu Gln Asn Gly Arg Cys Leu Arg Glu Ala Gln 385 390 395 400

Tyr Ser Met Leu Ala Thr Trp Arg Arg Thr Pro Arg Arg Glu Ala
405 410 415

Thr Leu Glu Leu Leu Gly Arg Val Leu Arg Asp Met Asp Leu Leu Gly 420 425 430

Cys Leu Glu Asp Ile Glu Glu Ala Leu Cys Gly Pro Ala Ala Leu Pro 435 440 445

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<211> 13

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<220>

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 (main sequence)

<220>

<221> UNSURE

<222> (4)

<223> identity of "Xaa" could not be determined

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1 5 10

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      (subsidiary sequence)
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cleavage peptide

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tcg cac aaa gga acc tac ttg tac aat gac tgt cca ggc ccg ggg cag Ser His Lys Gly Thr Tyr Leu Tyr Asn Asp Cys Pro Gly Pro Gly Gln 20 25 30	96
gat acg gac tgc agg gag tgt gag agc ggc tcc ttc aca gcc tca gaa Asp Thr Asp Cys Arg Glu Cys Glu Ser Gly Ser Phe Thr Ala Ser Glu 35 40 45	144
aac aac aag gatcc	158

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.010	00	
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12137	Altificial bequence	
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